Amendments to the Specification:

Please replace paragraph [00055] with the following amended paragraph:

[00055] **FIG. 15: IG20 Cells show increased specific activation of caspases upon TRAIL treatment** A) Initiator caspases - Hela IG20 cells and control cells treated with TRAIL for 1H, were stained, with flourochrome-conjugated peptide inhibitors of specific active caspases as indicated,fixed and analyzed by FACS. B) Caspase-8 cleavage - IG20 HeLa cells and control cells were treated with TRAIL for either 1H or 3H, lysed and immunoblotted for the 10 kDa cleaved product of active caspase-8 using the 6B6 monoclonal antibody. C) Caspase-3 activation - Hela IG20 cells and control cells untreated or treated with TRAIL or TNF–α and cycloheximide for 5 hours, were collected, fixed and stained with an active caspase-3 Phycoerythrin (PE) conjugated monoclonal antibody and subjected to FACS analyses. Above data are representative of 3 experiments. **LETD, AEVD and LEHD disclosed as SEQ ID NOS 10-12, respectively.**

Please replace paragraph [00073] with the following amended paragraph:

[00073] **FIG. 33: Mid si RNA region.** Total RNA was extracted from HeLa cells transduced with lentiviral vectors expressing control vector, Mid and DD siRNA regions after 24 and 48 hours post-transduction using Trizol (Life Technologies, Inc). 48 hours after transduction, the cells expressing the Mid siRNA region (5'-GTACCAGCTTCAGTCTTTC-3') **(SEQ ID NO: 1)** show knockdown of the IG20 gene as compared to the control vector and DD transduced cells. 0.8 μg of RNA was used in the Super-script one-step RT-PCR (Life Technologies, Inc) using F2-B2 primers, which amplify all isoforms of the IG20 gene. GAPDH was used as an internal control for the RT-PCR. The PCR products were separated on a 1% agarose gel.

Please replace paragraph [000161] with the following amended paragraph:

[000161] Human tissue samples were provided by the Cooperative Human Tissue Network (CHTN), which is funded by the National Cancer Institute. Highly pure intact full-length poly-A+mRNAs were directly isolated from various tissues using μMACS mRNA Isolation Kit (Miltenyi Biotec Inc., Auburn, CA) according to the manufacturer's protocol. Briefly, tissues were minced, lysed, mixed with the MicroBeads conjugated to Oligo (dT) and then loaded onto the μMACS magnetic columns. The columns were washed and the bound mRNAs eluted with hot (65°C) RNase-free water. Fifty ng mRNA from each sample was used in SuperScript-One- used; otherwise, protocols were identical. A first incubation at 50°C for 30 minutes was followed by incubation at 94°C for 2 minutes. Subsequent 30 cycles of PCR were carried out at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for variable time periods (as described herein), followed by a final incubation at 72°C for 7 minutes. For amplifying exons 13L and 16, F-1 and B-1 primer pair (5' CGG GAC TCTGAC TCC GAA CCT AC 3' **(SEQ ID NO: 2)** and 5' GCG GTT CAG CTT GCT CAG GAC 3' **(SEQ ID NO: 3)**, respectively) was used, with 1 minute extension time. For amplifying exon 21, F3453 and B3648 primer pair (5' AAG TGC CAC AGG AAA GGG TC 3' **(SEQ ID NO: 4)** and 5' TGC GCT GATCTG GGA CTT TT 3' **(SEQ ID NO: 5)**, respectively) was used, with 30 seconds extension time. For amplifying exon 26, F3944 and B4123 primer pair (5' AGC CAT GCA TAA AGG AGAAG 3' **(SEQ ID NO: 6)** and 5' GGT CCC ATA AAG TAG AAC GC 3' **(SEQ ID NO: 7)**, respectively) was used, with 30 seconds extension time. For amplifying exon 34, F4824 and B5092 primer pair (5' CTGCAG GTG ACC CTG GAA GGG ATC 3' **(SEQ ID NO: 8)** and 5' TGT ACC CGG GTC AGC TAG AGACAG GCC 3' **(SEQ ID NO: 9)**, respectively) was used, with 30 seconds extension time. All primers were used at 10 μM each. The resultant cDNAs were separated on 5% polyacrylamide gels (PAGE) and compared to molecular size markers to determine the product size.